



SEQUENCE LISTING

<110> Schein, Friedrich
Kerschbaumer, Randolph
Falkner, Falko-Guenter
Berner, Friedrich

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<140> US 09/661,992

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<170> PatentIn Ver. 2.1

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<220>

<221> Description of the artificial sequence:primer

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24

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Asp Gly Gly His Gly Tyr Gly Ser Ser Phe Asp Tyr
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Gln Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Val
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Gln Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Val
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<211> 9
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Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Val
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<210> 13

<211> 18

<212> PRT

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Val Tyr Gly Phe Gly Trp Gly Tyr Glu Val Asn Asp Tyr
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<110> 11

<111> 18

<112> PRT

<113> Artificial Sequence

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Glu Glu Glu Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Glu
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Glu Glu

<110> 13

<111> 18

<112> PRT

<113> Artificial Sequence

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<400> 12

Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
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Arg Arg

<210> 13

<211> 18

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<400> 13

Glu Tyr Gly Glu Gly Tyr Gly Glu Val Asn Glu Tyr Asp Glu Phe Glu
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Trp Glu

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Asp Glu

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<400> 15
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Arg Arg

<210> 16
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<212> PRT
<213> Artificial Sequence

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<400> 16
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1 5 10 15

Arg Arg

<210> 17
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
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<400> 17
Arg Arg Arg Gly Glu Tyr Gly Val Tyr Trp Asn Gly Asp Phe Tyr Arg
1 5 10 15

Arg Arg

<210> 16
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<221> Description of the artificial sequence:CDR3 region

<400> 16
Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 19
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<400> 19
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Arg Arg

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<400> 20
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Arg Arg

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<211> 18
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<210> 22
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<400> 22
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Arg Arg

<210> 23
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<212> PRT
<213> Artificial Sequence

<220>
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<400> 23
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Arg Arg

<210> 24
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
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<400> 24
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1 5 10 15

Arg Arg

<210> 25
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1 5 10 15

Arg Arg

<210> 26
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<400> 26
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1 5 10 15

Arg Arg

<210> 27
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<213> Artificial Sequence

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<400> 27
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1 5 10 15

Arg Arg

<210> 28
<211> 18
<212> PRT
<213> Artificial Sequence

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<400> 28
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1 5 10 15

Arg Arg

<210> 29
<211> 18
<212> PRT
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<400> 29
Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Ala Asp Arg

1 5 10 15

Arg Arg

<210> 30
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
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<400> 30
Arg Arg Arg Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Ala Arg
1 5 10 15

Arg Arg

<210> 31
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of the artificial sequence:CDR3 region

<400> 31
Arg Arg Arg Tyr Val Tyr Asn Gly Trp Gly Tyr Phe Glu Gly Ala Arg
1 5 10 15

Arg Arg

<210> 32
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
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<400> 32
Arg Arg Arg Glu Glu Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<210> 33
<211> 18
<212> PRT
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<400> 33

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Arg Arg

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.222>
.223> Description of the artificial sequence:CDR3 region

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<400> 37
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Arg Arg

<410> 38
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<413> Artificial Sequence

<420>
<423> Description of the artificial sequence:CDR3 region

<400> 38
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1 5 10 15

Arg Arg

<410> 39
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<412> PRT
<413> Artificial Sequence

<420>
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<400> 39
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Arg Arg

<410> 40
<411> 18
<412> PRT
<413> Artificial Sequence

<420>
<423> Description of the artificial sequence:CDR3 region

<400> 40
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Arg Arg

<410> 41
<411> 18
<412> FRT
<413> Artificial Sequence

<420>
<423> Description of the artificial sequence:CDR3 region

<400> 41
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Arg Arg

<210> 42
<211> 18
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<220>
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<400> 42
Arg Arg Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Glu Arg
1 5 10 15

Arg Arg

<210> 43
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
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<400> 43
Arg Arg Arg Gly Glu Tyr Gly Glu Tyr Trp Asn Gly Asp Phe Tyr Arg
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Arg Arg

<210> 44
<211> 13
<212> PRT
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<400> 44
Ser Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Val
1 5 10

<210> 45
<211> 14
<212> PRT
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<400> 45

Arg Glu Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Arg
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<211> 46

<211> 18

<212> PRT

<213> Artificial Sequence

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<400> 46

Phe Gly Val Gly Tyr Arg Gly Glu Thr Arg Asn Phe Asp Trp
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<211> 47

<211> 18

<212> PRT

<213> Artificial Sequence

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<223> Description of the artificial sequence:CDR3 region

<400> 47

Glu Glu Glu Glu Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Glu
5 10 15

Glu Glu

<211> 48

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:CDR3 region

<400> 48

Arg Arg Arg Glu Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Arg
1 5 10 15

Arg Arg

<211> 49

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:CDR3 region

<400> 49

Arg Arg Arg Phe Gly Val Gly Tyr Gly Glu Thr Asn Phe Asp Trp Arg
1 5 10 15

Arg Arg

<210> 50
<211> 57
<212> DNA
<213> Artificial Sequence

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<223> Description of the artificial sequence:primer

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<210> 51
<211> 56
<212> DNA
<213> Artificial Sequence

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<210> 52
<211> 56
<212> DNA
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<210> 53
<211> 56
<212> DNA
<213> Artificial Sequence

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<400> 53
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<210> 54
<211> 56
<212> DNA
<213> Artificial Sequence

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<210> 55

<211> 56
<212> DNA
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<210>
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<211> 56
<212> DNA
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<210>
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<211> 56
<212> DNA
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<211> 58
<212> DNA
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gtctcgcaaa ctgctggccca gccggccatg gccaggttc agtgcagca gctgg 56

<211> 59
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<211> 60
<212> DNA
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<220>

<223> Description of the artificial sequence:primer

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ttggccac

<211> 61

<211> 60

<212> DNA

<213> Artificial Sequence

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<223> Description of the artificial sequence:primer

<400> 61

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<211> 61

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:primer

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accgacagag ggcgcgccac ctgaaccgcc tccacctgag gagactgtga gactggtgcc 60

<410> 63

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:primer

<400> 63

accgacagag ggcgcgccac ctgaaccgcc tccacctgag gagacagtga ccagagtccc 60

<410> 64

<211> 60

<212> DNA

<213> Artificial Sequence

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<211> 60

<211> 60

<212> DNA

<213> Artificial Sequence

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<223> Description of the artificial sequence:primer

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410> 66
411> 59
412> DNA
413> Artificial Sequence

<223>

<223> Description of the artificial sequence:primer

410> 66
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410> 67
411> 59
412> DNA
413> Artificial Sequence

<223>

<223> Description of the artificial sequence:primer

4400> 67
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410> 63
411> 59
412> DNA
413> Artificial Sequence

<223>

<223> Description of the artificial sequence:primer

4400> 65
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410> 63
411> 59
412> DNA
413> Artificial Sequence

<223>

<223> Description of the artificial sequence:primer

4400> 69
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410> 70
411> 59
412> DNA
413> Artificial Sequence

<223>

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<210> 71

<211> 59

<212> DNA

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<210> 72

<211> 54

<212> DNA

<213> Artificial Sequence

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<215> Description of the artificial sequence:primer

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<210> 73

<211> 53

<212> DNA

<213> Artificial Sequence

<214>

<215> Description of the artificial sequence:primer

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<210> 74

<211> 41

<212> DNA

<213> Artificial Sequence

<214>

<215> Description of the artificial sequence:primer

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<210> 75

<211> 43

<212> DNA

<213> Artificial Sequence

<214>

<215> Description of the artificial sequence:primer

<400> 75

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<211> 76
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<212> DNA
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<400> 76
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<211> 77
<211> 42
<212> DNA
<213> Artificial Sequence

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<400> 77
aggtattct ggggcggccc gttttatttc caacttggtc cc 42

<211> 78
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<400> 78
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<211> 79
<211> 74
<212> DNA
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<223> Description of the artificial sequence:mychis 6

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cctcactaa taag 74

<211> 80
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<212> DNA
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atttttatt agtgatggtg atggatgatgt gccgccccat tcagatcctc ttctgagatg 60
agttttggtt ctgc 74

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 ccagaaaagg gttaaaagtg gatggggtgg ataaacacct aaactggaga gccaacatat 160
 gctgtgtaet tcaagggagc gtttgcttcc tctttggaaa cctctgctag cactgcttat 200
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 ctgatgtact atgcattcaa tgcctacaat ggagtccttg atcgcttcaa tggcagtgga 440
 tctggagcgg atttcacttt caccatcagc actgttcagg ctgaagacct ggcagtttat 480
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 aaacng 726

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 1 5 10 15
 Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asn Tyr 30
 20 25 30
 Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met 45
 35 40 45
 Gly Trp Ile Asn Thr Tyr Thr Gly Glu Pro Thr Tyr Ala Asp Asp Phe 60
 50 55 60
 Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Tyr 80
 65 70 75 80
 Leu Gln Ile Asn Asn Leu Lys Asn Glu Asp Thr Ala Thr Tyr Phe Cys 95
 85 90 95
 Ala Leu Tyr Gly Asn Ser Pro Lys Gly Phe Ala Tyr Trp Gly Gln Gly 110
 100 105 110
 Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly Gly Arg Ala 125
 115 120 125
 Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Lys Phe 140
 130 135 140
 Leu Leu Val Ser Ala Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser 160
 145 150 155 160
 Gln Ser Val Ser Asn Asp Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln

165

170

175

Ser Pro Lys Leu Leu Met Tyr Tyr Ala Ser Asn Arg Tyr Thr Gly Val
160 165 190

Pro Asp Arg Phe Thr Gly Ser Gly Tyr Gly Thr Asp Phe Thr Phe Thr
195 200 205

Ile Ser Thr Val Gln Ala Glu Asp Leu Ala Val Tyr Phe Cys Gln Gln
210 215 220

Asp Tyr Gly Ser Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
225 230 235 240

Lys Arg

4110-83

4111-847

4112-8NA

4113- Artificial Sequence

4120-

4123- Description of the artificial sequence:scFv region

4400-83

gaagtgagc tgggtggagtc tggggggaggg ctagtgaagc ctggagggtc cctgaaaactc 60
tctctgtcag cctctggatt cactttcagt acctatacca tgtcttgggt ccgcagagct 120
cgggagaaga ggcctggagtg ggtcgcaacc attagtagtg gtggtagtta cactactat 180
cgaacagtg tgaggggccc attcaccatc tccagagaca atgccaagaa caccctgtac 240
ctgcaatga gcagtctgaa gtctgaggac acagccatgt attactgtac aagagatggg 300
ggacagggt acggtagtag ctctgactac tggggccaag gcaccactct cacagtctcc 360
tcaggtggag ggggttcagg tggggggccc tctggcggtg ggggatcgca aattgtgtc 420
acccagtctc cactctccct gctgtcagt ctggagatc aagcctccat ctcttgaga 480
ctagtcaga gcattgtaca tagtaatgga aacacctatt tagaatggta cctgcagaaa 540
tcagccagt ctccaaagct cctgatctac aaagtctcca accgattttc tggggtccca 600
gcacaaattca gtggcagttg atcagggaca gatttcacac tcaagatcag cagagtggag 660
gtgaggatc tgggagttta ctactgcttt caaggttcac atgttcogtg gacgttcggt 720
gagtcacca agctggaaat caaacgg 747

4110-84

4111-249

4112-PRT

4113- Artificial Sequence

4120-

4123- Description of the artificial sequence:scFv region

4400-84

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Thr Tyr
20 25 30

Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Ser Gly Gly Ser Tyr Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Arg Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80
 Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
 85 90 95
 Thr Arg Asp Gly Gly His Gly Tyr Gly Ser Ser Phe Asp Tyr Trp Gly
 100 105 110
 Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
 115 120 125
 Arg Ala Ser Gly Gly Gly Gly Ser Gln Ile Val Leu Thr Gln Ser Pro
 130 135 140
 Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg
 145 150 155 160
 Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu Trp
 165 170 175
 Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val
 180 185 190
 Ser Asn Arg Phe Ser Gly Val Pro Asp Lys Phe Ser Gly Ser Gly Ser
 195 200 205
 Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu
 210 215 220
 Gly Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Trp Thr Phe Gly
 225 230 235 240
 Gly Gly Thr Lys Leu Glu Ile Lys Arg
 245

<210> 85

<211> 247

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence: scFv region.

<200> 85

ttgtgcagc ttccaggagtc aggggggagc ttagtgaagc ctggagggtc cctgaaactc 60
 tctgtgcag cctctggatt cactttcagt agctatacca tgtcttgggt tccgcagact 120
 ctggagaaga ggtctggagt gctcgcaacc attagttagt gtggtagttc cactacttat 180
 ccagacagt tgaagggccg attcaccatc tccagagaca atgccaagaa caccctgtac 240
 ctgcaaatga gcagctctgag gtctgaggac acagccatgt attactgtac aagagagggg 300
 ggtggtttca cgttcaactg gacttccgat gtctggggcg cagggaactct ggtcactgtc 360
 tctgcaggtg gagggggttc aggtggggcg gctctggcg gtgggggata gaaaaatgtg 420
 ctcccccagt ctccagcttc ttgtgctgtg tctctagggc agagggtcac catatcctgc 480
 agagccagtg aaagtgttga tagttatggc tataatttta tgcactggta ccagcajata 540
 ccaggacagc cccccaaact ctcctctat cgtgcaccca acctagagtc tgggatccct 600
 ggcaggttca gtggagtggt gctcaggaca caattcaccc tcaccattaa tctgtgtgag 660
 gctgatgatg ttgcaacctc ttactgtcag caaagtaatg aggatccgct caggttcagg 720
 actgggacca gactggaaat aaaacgg 747

<210> 86

<211> 249

<212> FRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 66

Glu Val Gln Leu Gln Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
35 40 45

Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr Tyr Tyr Pro Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Ser Ser Leu Arg Ser Glu Asp Thr Ala Met Tyr Tyr Cys
85 90 95

Thr Arg Glu Gly Gly Gly Phe Thr Val Asn Trp Tyr Phe Asp Val Trp
100 105 110

Gly Ala Gly Thr Leu Val Thr Val Ser Ala Gly Gly Gly Gly Ser Gly
115 120 125

Gly Arg Ala Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser
130 135 140

Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys
145 150 155 160

Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly Tyr Asn Phe Met His Trp
165 170 175

Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala
180 185 190

Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
195 200 205

Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val
210 215 220

Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp Pro Leu Thr Phe Gly
225 230 235 240

Thr Gly Thr Arg Leu Glu Ile Lys Arg
245

<210> 87

<211> 747

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 87

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caggagaaga ggtctggagt ggtcgcaacc attagtatgt gtgttagttc cacttactat 147  
ccagacagt tgaaggggccg attcaccatc tccagagaca atgccaagaa caccctgtac 147  
ctgcaaatga gcagttctgaa gtctgaggac acagccatgt atcactgtac aagagagggg 173  
gtgtgttatt acgtcaactg gtacttctgat gtctggggcg caggcaaccac tctcagagtc 173  
tctcagagtg gaggggggtc aggtggggcg gctctggcg gtgggggacg ggcattgtag 173  
ctcaccagct ctcagagctc tttgtctgtg tctctaggcg agaggggcac catatctgt 173  
agagccagtg aaagtgttga tagttatggo aagagtttta tgcactggta ccagcagaaa 173  
ccagggcagc cacccaaaact cctcattctat cgtgcaccca acctagaatc tgggacccct 173  
ccaggttcca gtggcagtg gtctaggaca gacttcaccc tcaccattaa tctctgggag 173  
gtgtgtgtgt ttgcnacctt ttaactgtcag caaagttaat aggtacccct cactgtcggt 173  
gtgtggacca gactggaat aaaaagg 173
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<210> 88

<211> 249

<212> FRT

<213> Artificial Sequence

220

223> Description of the artificial sequence:scFv region

400> 88

```
Glu Val Gln Leu Gln Ser Gly Gly Gly Leu Val Lys Pro Gly Gly  
1 5 10 15  
Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr  
20 25 30  
Thr Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val  
35 40 45  
Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr Tyr Tyr Pro Asp Ser Val  
50 55 60  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr  
65 70 75 80  
Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr His Cys  
85 90 95  
Thr Arg Glu Gly Gly Gly Tyr Tyr Val Asn Trp Tyr Phe Asp Val Trp  
100 105 110  
Gly Ala Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Gly Ser Gly  
115 120 125  
Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser  
130 135 140  
Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr Ile Ser Cys  
145 150 155 160  
Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly Lys Ser Phe Met His Trp  
165 170 175  
Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala  
180 185 190  
Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
```

195

200

205

Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro Val Glu Ala Asp Asp Val
210 215 220

Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu Asp Pro Leu Thr Phe Gly
225 230 235 240

Ala Gly Thr Arg Leu Glu Ile Lys Arg
245

<210> 9

<211> 1199

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 9

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atggcgagg tgaagctgg ggagttctgg ggagcttag tgaagctgg agggctccctg 120
aacctctct ggcagctc tgatctact tccagttagc ataccatgtc ttgggttcgc 180
cagatccgg aagagaggtt gtagtgggtc gaaacatta gtagtggngg tagttccacc 240
tactatccag aagatgtgaa ggcgcgattc accatctcc gagacattgc caagaacacc 300
ctgtatctgc aatgagcag ttgaggttc gaggacacag caatgtatta ctgtacaaga 360
gagggggtg gttccactt caactgggtc ttgaggtct ggagcggaag aactccagtc 420
aaggttctct caggtggagg cgttccagtc gggcgcgct ctgggggtg cggatccggc 480
atgtgttga caggtctcc agttctctt gctgtctctc tagggcag aggccaccata 540
tctgtcagag cagtgaaag ttctgataat tatgtctata attttatgca ctggtatcag 600
cagatccag gacagccacc caaactcttc atctatctgt caccacact agagtctgg 660
atccctgcca gttccagttg cagtgggtct aggcagact tcaccctcac cattaactt 720
ggcgaggctg abgatgtgc aactattac ttccagcaaa gtaatgagja tccgtccag 780
tccggtactg gaaacagact gaaataaaaa cggcgcgcc cagcccgggc aacagaaaatg 840
ctggtctcgg aaaaacgggc tctccagggc gatattactt cacccgcgcg tcttcgcctt 900
tcaacgggtg accagactgc cgtctcgtct gathctctta tccgataaac tgcataaaat 960
attatttgc tgaatggga ttggatggg tactccgaaa ctactgcctc acgtaatttt 1020
gggaaggtg cggcgcgctt tcttaaaagt atagatgcct caccgcttac cgggcaatat 1080
atccactatg cgttgatata aaaaacgggc aaacggact cgtccaccja ctcggttga 1140
ctggcaacgg cctggccaac cgtgtcaaaa tcttcaacg ggcgctggg cgtcgataat 1200
cagcaaaaag atccaccaac gattctggaa atggcaaaa cgcaggtctt ggcgaccggt 1260
aagttctcta cggcagagtc gcaggatgcc accgcgctg cgtcggtggc acatgtgacc 1320
tccgcgaatc gtaacggctc gagcgcgacc agtgaaaaat gtcgggttaa cgtctctgaa 1380
aaagcgjjaa aaggtatgat taccgaacag ctgttcaacg ctcggtccja cgttaacgct 1440
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ctjcggtjaac aggcacaggg gcgtgggttat cagttgggtg gcgatgctgc ctcaactgat 1560
tgggtgacgg aagcgaatca gcaaaaaacc ctgcttggcc tgtttgctga cggcaatatg 1620
cagtcggctt ggtcagjacc gaaagcaacg tactatggja atatcgataa gcccgagtc 1680
aactgtacgg caaatccgca acgtaatgac agtgtaccaa cctggcgcca gatgaccgac 1740
aaagccattg aattgttgag taaaaatgag aaaggctttt tctgcgaagt tgaagggtgg 1800
tcaatcgata aacaggtatc tctgcgaat cctgttgggc aaattggcga gacggtcgat 1860
ctcgatgaag cgtacaaag ggcgctggja ttctctaaaa aggagggtaa caogctggtc 1920
atagttacgg ctgatacgg ccacgcgcgc tagattgttg cgcgggatac caaagctccg 1980
ggcttcaacc aggcgctaaa taccaaaat ggcgcagtgat tgggtgatgac ttacggggaac 2040
tcggaagagg attcacaaga acataccggc agtcagttgc gtattcgggc gtatggcccg 2100
catcccgcca atgttctgtg actgacccgc cagaccgata tctctacac catgaaagcc 2160
gctctcgggg atatcgaca ccatcaccat caccattaa 2199

```

<210> 90

<211> 732

<212> BHT

42130 Artificial Sequence

42130

42130 Description of the artificial sequence:scFv region

4411-46

Met	Lys	Tyr	Leu	Leu	Pro	Thr	Ala	Ala	Ala	Gly	Leu	Leu	Leu	Leu	Ala	1	5	10	15
Ala	Gln	Pro	Ala	Met	Ala	Glu	Val	Lys	Leu	Val	Glu	Ser	Gly	Gly	Gly	20	25	30	
Leu	Val	Lys	Pro	Gly	Gly	Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser	Gly	35	40	45	
Phe	Thr	Phe	Ser	Ser	Tyr	Thr	Met	Ser	Trp	Val	Arg	Gln	Thr	Pro	Glu	50	55	60	
Lys	Arg	Leu	Glu	Trp	Val	Ala	Thr	Ile	Ser	Ser	Gly	Gly	Ser	Ser	Thr	65	70	75	80
Tyr	Tyr	Pro	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	85	90	95	
Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Ser	Ser	Leu	Arg	Ser	Glu	Asp	100	105	110	
Thr	Ala	Met	Tyr	Tyr	Cys	Thr	Arg	Glu	Gly	Gly	Gly	Phe	Thr	Val	Asn	115	120	125	
Trp	Tyr	Phe	Asp	Val	Trp	Gly	Ala	Gly	Thr	Ser	Val	Thr	Val	Ser	Ser	130	135	140	
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Arg	Ala	Ser	Gly	Gly	Gly	Gly	Ser	Asp	145	150	155	160
Ile	Val	Leu	Thr	Gln	Ser	Pro	Ala	Ser	Leu	Ala	Val	Ser	Leu	Gly	Gln	165	170	175	
Arg	Ala	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Glu	Ser	Val	Asp	Ser	Tyr	Gly	180	185	190	
Tyr	Asn	Phe	Met	His	Trp	Tyr	Gln	Gln	Ile	Pro	Gly	Gln	Pro	Pro	Lys	195	200	205	
Leu	Leu	Ile	Tyr	Arg	Ala	Ser	Asn	Leu	Glu	Ser	Gly	Ile	Pro	Ala	Arg	210	215	220	
Phe	Ser	Gly	Ser	Gly	Ser	Arg	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Asn	Pro	225	230	235	240
Val	Glu	Ala	Asp	Asp	Val	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Asn	Glu	245	250	255	
Asp	Pro	Leu	Thr	Phe	Gly	Thr	Gly	Thr	Arg	Leu	Glu	Ile	Lys	Arg	Ala	260	265	270	
Ala	Ala	Ala	Arg	Ala	Pro	Glu	Met	Pro	Val	Leu	Gln	Asn	Arg	Ala	Ala	275	280	285	
Gln	Gly	Asp	Ile	Thr	Ala	Pro	Gly	Gly	Ala	Arg	Arg	Leu	Thr	Gly	Asp	290	295	300	

Gln Thr Ala Ala Leu Arg Asp Ser Leu Ser Asp Lys Pro Ala Lys Asn
 303 310 315 320
 Ile Ile Leu Leu Ile Gly Asp Gly Met Gly Asp Ser Glu Ile Thr Ala
 325 330 335
 Ala Arg Asn Tyr Ala Glu Gly Ala Gly Gly Phe Phe Lys Gly Ile Asp
 340 345 350
 Ala Leu Pro Leu Thr Gly Gln Tyr Thr His Tyr Ala Leu Asn Lys Lys
 355 360 365
 Thr Gly Lys Pro Asp Tyr Val Thr Asp Ser Ala Ala Ser Ala Thr Ala
 370 375 380
 Trp Ser Thr Gly Val Lys Thr Tyr Asn Gly Ala Leu Gly Val Asp Ile
 385 390 395 400
 His Glu Lys Asp His Pro Thr Ile Leu Glu Met Ala Lys Ala Ala Gly
 405 410 415
 Leu Ala Thr Gly Asn Val Ser Thr Ala Glu Leu Gln Asp Ala Thr Pro
 420 425 430
 Ala Ala Leu Val Ala His Val Thr Ser Arg Lys Cys Tyr Gly Pro Ser
 435 440 445
 Ala Thr Ser Glu Lys Cys Pro Gly Asn Ala Leu Glu Lys Gly Gly Lys
 450 455 460
 Gly Ser Ile Thr Glu Gln Leu Leu Asn Ala Arg Ala Asp Val Thr Leu
 465 470 475 480
 Gly Gly Gly Ala Lys Thr Phe Ala Glu Thr Ala Thr Ala Gly Glu Trp
 485 490 495
 Gln Gly Lys Thr Leu Arg Glu Gln Ala Gln Ala Arg Gly Tyr Gln Leu
 500 505 510
 Val Ser Asp Ala Ala Ser Leu Asn Ser Val Thr Glu Ala Asn Gln Gln
 515 520 525
 Lys Pro Leu Leu Gly Leu Phe Ala Asp Gly Asn Met Pro Val Arg Trp
 530 535 540
 Leu Gly Pro Lys Ala Thr Tyr His Gly Asn Ile Asp Lys Pro Ala Val
 545 550 555 560
 Thr Cys Thr Pro Asn Pro Gln Arg Asn Asp Ser Val Pro Thr Leu Ala
 565 570 575
 Gln Met Thr Asp Lys Ala Ile Glu Leu Leu Ser Lys Asn Glu Lys Gly
 580 585 590
 Phe Phe Leu Gln Val Glu Gly Ala Ser Ile Asp Lys Gln Asp His Ala
 595 600 605
 Ala Asn Pro Cys Gly Gln Ile Gly Glu Thr Val Asp Leu Asp Glu Ala
 610 615 620
 Val Gln Arg Ala Leu Glu Phe Ala Lys Lys Glu Gly Asn Thr Leu Val
 625 630 635 640

Ile Val Thr Ala Asp His Ala His Ala Ser Gln Ile Val Ala Pro Asp
648 651 655

Thr Lys Ala Pro Gly Leu Thr Gln Ala Leu Asn Thr Lys Asp Gly Ala
660 665 670

Val Met Val Met Ser Tyr Gly Asn Ser Glu Glu Asp Ser Gln Gln His
675 680 685

Thr Gly Ser Gln Leu Arg Ile Ala Ala Tyr Gly Pro His Ala Ala Asn
690 695 700

Val Val Gly Leu Thr Asp Gln Thr Asp Leu Phe Tyr Thr Met Lys Ala
705 710 715 720

Ala Leu Gly Asp Ile Ala His His His His His His
725 730

<210> 81

<211> 978

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 91

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Atgaaatacc tattgcaatc ggcagccgct ggattgttat tactcggcgc ccagccggcc 60
atggcgggagg tgaagctggg ggagctctgg ggaggcttag tgaagctgg agggctccctg 120
aaactctcct ggcagccctc tggattcaat tttagtagct ataccatgtc ttgggttcgc 180
caactccggg agaagaggct ggagtggttc gcaaccatta gtatggngg tagttccacc 240
taattccag acagctgtga ggcccgatcc accatctcca gagacaatgc caagaacacc 300
ctgtacctgc aaatgagcag cctgaggtct gaggacacag ccattgtatta ctgtacaaga 360
gaggggggtg gtttcacagt caactggtag ttgatgtct gggggcaggg aacctcagtc 420
acagctctct caggtggagg cggttcaggt gggcgcgcct ctggcgggtg cggatcggac 480
attgtgctga cacagctcc agctctcttg gctgtgtctc tagggcagag ggccaccata 540
tcctgcagag ccagtgaag tttgatagt cctggctata atttcatgca ctggtatcag 600
cagataccag gacagccacc caaactctct atctatcttg catccaaact agagtctggg 660
atccctgcca ggttcagtgg cagtggtctc aggaacagct tcacccctcc cattaatct 720
gtcggaggtg atgatgttc aacctattac tctcagcaaa gtaatgagga tccgtccag 780
ttgggtactg ggaccagact ggaataaaaa cgggcggcgc caccgaagcc ttccactccg 840
cccggtctct ccggtatgaa acagctggaa gacaaagtag aggagctctc tagcaagaac 900
taacatctag aaaaagaggt agctcgtctg aaaaagcttg ttggtgaacg tgggtgtcac 960
catcaccatc accattaa 978

```

<310> 82

<311> 325

<312> PRT

<313> Artificial Sequence

<410>

<413> Description of the artificial sequence:scFv region

<400> 92

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala Glu Val Lys Leu Val Glu Ser Gly Gly Gly
20 25 30

Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly

35

40

45

Phe Thr Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu
50 55 60

Lys Arg Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr
65 70 75 80

Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
85 90 95

Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp
100 105 110

Thr Ala Met Tyr Tyr Cys Thr Arg Glu Gly Gly Gly Phe Thr Val Asn
115 120 125

Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Ser Val Thr Val Ser Ser
130 135 140

Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp
145 150 155 160

Ile Val Leu Thr Gln Xaa Pro Ala Ser Leu Ala Val Ser Leu Gly Gln
165 170 175

Arg Ala Thr Ile Ser Cys Arg Ala Ser Glu Ser Val Asp Ser Tyr Gly
180 185 190

Tyr Asn Phe Met His Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys
195 200 205

Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg
210 215 220

Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro
225 230 235 240

Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu
245 250 255

Asp Pro Leu Thr Phe Gly Thr Gly Thr Arg Leu Glu Ile Lys Arg Ala
260 265 270

Ala Ala Pro Lys Pro Ser Thr Pro Pro Gly Ser Ser Arg Met Lys Gln
275 280 285

Leu Glu Asp Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu
290 295 300

Asn Glu Val Ala Arg Leu Lys Lys Leu Val Gly Glu Arg Gly Gly His
305 310 315 320

His His His His His
325

<10> 93

<11> 2190

<12> DNA

<13> Artificial Sequence

<20>

<223> Description of the artificial sequence:scFv region

<400> 94

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adattttcct gcaaaagotto tggctacgca ttcagtagct cttggatgaa ctgggtgaa 181
tagaggccctg gacagggtct gtagtggatt ggcaggatct atctggaaa tggagatact 241
aactacaatg ggaagttcaa gggcaaggcc acactgactg cagacaaatc ctccagcaca 301
gactacatgc agctcagcag cctgacctct gtggactctg cggcttatct ctgtgcagat 361
ggttaacgtat attactatgc tatggactac tgggttcaag gaacctcagt caccgtctct 421
tcagggtggag ggggttcagg tggggcgccc cctgggggtg ggggatcgaa aattgtctct 481
accacgtctc ctgcttctct agctgtatct ctggygcaga gggccacct ctcatgcagg 541
gccagcaaaa ggttcagtag atctggctat agttatatgc actggtacca acagaaacca 601
ggacaggctac ccaaaactct cttctatctt gcatccaaac tagaactct gggtccctgc 661
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gaaaaacggg ctgctcaggg cgtatattact gacccggcg gtgctcgccg ttttaacggg 901
gacacagactg ccgctctcg cgtattctctt agcgtataaa ctgcaaaaaa tattattttg 961
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gctgtgtcaa cgggtgtcaa aabttataac gggcggtggg ggttcgatat tcaagaaaaa 1200
gatcacccaa cgtattctga aatggcaaaa gcgpcaggtc tggcgacggg taaggtttct 1260
acbgcagagt tgcaggatgc cagcccgctt ggcgtgtgg cactatgtgc ctccggcaaa 1320
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gaaaaaacct ttgtgaaa cggcaacgct ggtgaatgg agggaaaaac gctgctgaa 1500
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tagcgatc agcaaaaaac cctgcttggc ctgtttggc agggcaatat ggcagtgcgc 1620
tagctagjac cgaagcaac gtaaccatgg aatatcgata agcccgagct cactgtacg 1680
caaatccg cactgaatga cagtgtacca accctggggt agatgacga caaagccatt 1740
gaattgttga gtaaaaaatg gaaaggcttt ttcctgcaag ttgaaggtgc gtcactcgat 1800
aaacaggatc atgctcgga tcttctgtgg caaattgggt agacggtcga tctcgatgaa 1860
gctgtacaa cggcgctgga attcgctaaa aaggagggtt acacgctggt catagtccac 1920
gctgacacg ccacgcccag ccagattgtt agcccgata ccaaaagctc gggcctcacc 1980
cagcgctaaa ataccaaa gggcgagtg atggtgatga gttacgggaa ctccgaagg 2040
gattcacaa aacataccg cagtcagttg cgtattgggt cgtatggccc gcatgcgcgc 2100
aattgtgttg gaactgacga ccagacgat ctctctaca ccattgaaagc cgtctggggg 2160
gattatgcac accatcaca tcaaccattaa 2190

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<110> 94

<111> 729

<112> FRT

<113> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 94

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Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala
1           5           10          15

Ala Gln Pro Ala Met Ala Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
20          25          30

Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
35          40          45

Tyr Ala Phe Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly
50          55          60

```

Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr
 65 70 75 80
 Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys
 85 90 95
 Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp
 100 105 110
 Ser Ala Val Tyr Phe Cys Ala Asp Gly Asn Val Tyr Tyr Tyr Ala Met
 115 120 125
 Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly
 130 135 140
 Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Gln Ile Val Leu
 145 150 155 160
 Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr
 165 170 175
 Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr
 180 185 190
 Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
 195 200 205
 Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly
 210 215 220
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu
 225 230 235 240
 Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Arg
 245 250 255
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Ala
 260 265 270
 Arg Ala Pro Glu Met Pro Val Leu Glu Asn Arg Ala Ala Gln Gly Asp
 275 280 285
 Ile Thr Ala Pro Gly Gly Ala Arg Arg Leu Thr Gly Asp Gln Thr Ala
 290 295 300
 Ala Leu Arg Asp Ser Leu Ser Asp Lys Pro Ala Lys Asn Ile Ile Leu
 305 310 315 320
 Leu Ile Gly Asp Gly Met Gly Asp Ser Glu Ile Thr Ala Ala Arg Asn
 325 330 335
 Tyr Ala Glu Gly Ala Gly Gly Phe Phe Lys Gly Ile Asp Ala Leu Pro
 340 345 350
 Leu Thr Gly Gln Tyr Thr His Tyr Ala Leu Asn Lys Lys Thr Gly Lys
 355 360 365
 Pro Asp Tyr Val Thr Asp Ser Ala Ala Ser Ala Thr Ala Trp Ser Thr
 370 375 380
 Gly Val Lys Thr Tyr Asn Gly Ala Leu Gly Val Asp Ile His Glu Lys
 385 390 395 400

Asp His Pro Thr Ile Leu Glu Met Ala Lys Ala Ala Gly Leu Ala Thr
 405 410 415
 Gly Asn Val Ser Thr Ala Glu Leu Gln Asp Ala Thr Pro Ala Ala Leu
 420 425 430
 Val Ala His Val Thr Ser Arg Lys Cys Tyr Gly Pro Ser Ala Thr Ser
 435 440 445
 Glu Lys Cys Pro Gly Asn Ala Leu Glu Lys Gly Gly Lys Gly Ser Ile
 450 455 460
 Thr Glu Gln Leu Leu Asn Ala Arg Ala Asp Val Thr Leu Gly Gly Gly
 465 470 475 480
 Ala Lys Thr Phe Ala Glu Thr Ala Thr Ala Gly Glu Trp Gln Gly Lys
 485 490 495
 Thr Leu Arg Glu Gln Ala Gln Ala Arg Gly Tyr Gln Leu Val Ser Asp
 500 505 510
 Ala Ala Ser Leu Asn Ser Val Thr Glu Ala Asn Gln Gln Lys Pro Leu
 515 520 525
 Leu Gly Leu Phe Ala Asp Gly Asn Met Pro Val Arg Trp Leu Gly Pro
 530 535 540
 Lys Ala Thr Tyr His Gly Asn Ile Asp Lys Pro Ala Val Thr Cys Thr
 545 550 555 560
 Pro Asn Pro Gln Arg Asn Asp Ser Val Pro Thr Leu Ala Gln Met Thr
 565 570 575
 Asp Lys Ala Ile Glu Leu Leu Ser Lys Asn Glu Lys Gly Phe Phe Leu
 580 585 590
 Gln Val Glu Gly Ala Ser Ile Asp Lys Gln Asp His Ala Ala Asn Pro
 595 600 605
 Cys Gly Gln Ile Gly Glu Thr Val Asp Leu Asp Glu Ala Val Gln Arg
 610 615 620
 Ala Leu Glu Phe Ala Lys Lys Glu Gly Asn Thr Leu Val Ile Val Thr
 625 630 635 640
 Ala Asp His Ala His Ala Ser Gln Ile Val Ala Pro Asp Thr Lys Ala
 645 650 655
 Pro Gly Leu Thr Gln Ala Leu Asn Thr Lys Asp Gly Ala Val Met Val
 660 665 670
 Met Ser Tyr Gly Asn Ser Glu Glu Asp Ser Gln Glu His Thr Gly Ser
 675 680 685
 Gln Leu Arg Ile Ala Ala Tyr Gly Pro His Ala Ala Asn Val Val Gly
 690 695 700
 Leu Thr Asp Gln Thr Asp Leu Phe Tyr Thr Met Lys Ala Ala Leu Gly
 705 710 715 720
 Asp Ile Ala His His His His His
 725

<210> 95
 <211> 969
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> Description of the artificial sequence:scFv region

<400> 95
 atgaaatacc tattgootac ggcagccgct ggattgttat tactcggggc ccagccggcc 61
 atggcggagg tttagcttca gcagtctgga cctgagctgg tgaagccgg ggctccagtg 121
 aagatttccct gcaaaagcttc tggtacgca ttccagtact cttggatgaa ctgggtgaag 181
 cagaggcctg gacagggtct tgagtggatt ggaaggattt atctggaaa tggagatact 241
 aactacaatg ggaagttcaa gggcaaggcc acactgactg cagacaaatc ctccagcaca 301
 gctacatgc agtcagcag cctgacctct gtggactctg cgtctatatt ctgtccagat 361
 ggtaacgtat attactatgc tatggactac tggggtaag gaaactcagt cactgtctcc 421
 tcaggtggag gctgttcagg tggcgcgcc tctggcggtg ggggatcgca aattgttctc 481
 acccagtctc ctgtctcctt agctgtatct ctggggcaga gggccacct ctcatgcagg 541
 gcaagcaaaa gtgtcagtac atctggctat agttatatgc actggtacca acagaaacca 601
 gcaagccac ccaaaactct catctatctt gcacccaacc tagaatctgg ggtccctgcc 661
 aggtccagtg gcagtgggtc tgggacagac ttacacctca acatccatcc tgtggaggag 721
 caggtatgct gaacctatta ctgtcagcac agtagggagc ttctcggac gttcgttggc 781
 cgcacaaagc tggaaatcaa acggcgggcc gcaccgaagc cttccactcc gcccggtct 841
 tccctatga accagctgga agacaaagta gaggagctcc ttgcaagaa ctaccatcta 901
 gaaaacgagg tagctcgtct gaaaaagctt gttggtgaac gtggtggtca ccataccat 961
 caccattaa 969

<210> 96
 <211> 322
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> Description of the artificial sequence:scFv region

<400> 96
 Met Lys Tyr Leu Ieu Pro Thr Ala Ala Ala Gly Ieu Ieu Leu Leu Ala
 1 5 10 15
 Ala Gln Pro Ala Met Ala Glu Val Gln Ieu Gln Gln Ser Gly Pro Glu
 20 25 31
 Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Iys Ala Ser Gly
 35 40 45
 Tyr Ala Phe Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly
 50 55 60
 Gln Gly Ieu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr
 65 70 75 80
 Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys
 85 90 95
 Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp
 100 105 110
 Ser Ala Val Tyr Phe Cys Ala Asp Gly Asn Val Tyr Tyr Tyr Ala Met
 115 120 125
 Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly

130	135	140
Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Gln Ile Val Leu		
145	150	155
Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr		
165	170	175
Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr		
180	185	190
Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile		
195	200	205
Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly		
210	215	220
Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu		
225	230	235
Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Arg		
245	250	255
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Pro		
260	265	270
Lys Pro Ser Thr Pro Pro Gly Ser Ser Arg Met Lys Gln Leu Glu Asp		
275	280	285
Lys Val Glu Glu Leu Leu Ser Lys Asn Tyr His Leu Glu Asn Glu Val		
290	295	300
Ala Arg Leu Lys Lys Leu Val Gly Glu Arg Gly Gly His His His His		
305	310	315
		320
His His		

<210> 97
 <211> 270
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of the artificial sequence:scFv region

<400> 97
 caggaaacag ctatgaccat gattaagcga agcttccatg aaaattctat ttcaaggaga 60
 cagtcataat gaaataaccta ttgcctacgg cagccgctgg attgttatta ctgcgggcc 120
 agccggccat ggcccaggtg cagctgcagg cgcgcctgca ggtcgacctc gagatcaaac 180
 ggcgggcgc agaacaaaaa ctatctcag aagaggatct gaatggggcg gcacatcacc 240
 atcaccatca ctaataagaa ttaactggcc 270

<210> 98
 <211> 61
 <212> FRT
 <213> Artificial Sequence

<220>
 <223> Description of the artificial sequence:scFv region

<400> 96

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln Ala Arg Leu Gln Val
20 25 30

Asp Leu Glu Ile Lys Arg Ala Ala Ala Gln Gln Lys Leu Ile Ser Gln
35 40 45

Glu Asp Leu Asn Gly Ala Ala His His His His His His
50 55 60

<210> 99

<211> 666

<212> DNA

<213> Artificial Sequence

121

122 Description of the artificial sequence:scFv region.

<400> 99

cgagatacc tattgcttac ggcagcgcgt ggattgttat tactcggggc ccagccgggc 20
cgagccgagg tgaagctggt ggagctctgg ggaggttag tgaagcctgg agggctccctg 120
aaactctcct gtgcagcctc tggattcact ttcagttagc ataccatgtc ttgggttcgc 180
cagactccgg agaagagggt ggagtggttc gcaaccatta gtagtggngg tagttccacc 240
tactatccag acagtgtgaa gggccgatto accatctcca gagacaatgc caagaacacc 300
cgttaccctg aatgagcag tctgaggtct gaggacacag ccattgtatta ctgtacaaga 360
gagggggggt gtatcacctt caactggtao ttcatgtct gggggcaggg aacctcagtc 420
aacgtctcct caggtggagg cggttccaggt gggcgggctt ctggcgggtg cggatccggc 480
attgtgctga cacagtctcc agcttctttg gctgtgtctc tagggcagag ggcaccata 540
tctgtcagag ccagtgaag tttgatagt tatggtata attttatgca ctgggtatcag 600
cagataccag gacagccacc caaatctctc atcatcgtg catccaaact agagtctggg 660
atccctgcca ggttcagtyg cagtgggtct aggaagact ccacctccac cattaatct 720
gaggaggctg atgattcttg aacctattac tgtacgaaa gtaatgagga tccgctcag 780
tccgtactg ggaccagct ggaataaaaa cggcggcgc cagaacaaaa actcatctca 840
gaagaggatc tgaatggggc ggcacatcac catcacatc actaataa 888

<210> 100

<211> 294

<212> PRT

<213> Artificial Sequence

<400>

123 Description of the artificial sequence:scFv region

<400> 100

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala Glu Val Lys Leu Val Glu Ser Gly Gly Gly
20 25 30

Leu Val Lys Pro Gly Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly
35 40 45

Phe Thr Phe Ser Ser Tyr Thr Met Ser Trp Val Arg Gln Thr Pro Glu
50 55 60

Lys Arg Leu Glu Trp Val Ala Thr Ile Ser Ser Gly Gly Ser Ser Thr
65 70 75 80

Tyr Tyr Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn
 85 91 95
 Ala Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Arg Ser Glu Asp
 100 105 110
 Thr Ala Met Tyr Tyr Cys Thr Arg Gln Gly Gly Gly Phe Thr Val Asn
 115 120 125
 Trp Tyr Phe Asp Val Trp Gly Ala Gly Thr Ser Val Thr Val Ser Ser
 130 135 140
 Gly Gly Gly Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Asp
 145 150 155 160
 Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln
 165 170 175
 Arg Ala Thr Ile Ser Cys Arg Ala Ser Gln Ser Val Asp Ser Tyr Gly
 180 185 190
 Tyr Asn Phe Met His Trp Tyr Gln Gln Ile Pro Gly Gln Pro Pro Lys
 195 200 205
 Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Ala Arg
 210 215 220
 Phe Ser Gly Ser Gly Ser Arg Thr Asp Phe Thr Leu Thr Ile Asn Pro
 225 230 235 240
 Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Ser Asn Glu
 245 250 255
 Asp Pro Leu Thr Phe Gly Thr Gly Thr Arg Leu Glu Ile Lys Arg Ala
 260 265 270
 Ala Ala Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala
 275 280 285
 His His His His His
 290

<210> 101
 <211> 876
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of the artificial sequence:scFv region

<400> 101
 atgaaatacc tattgcttac ggcagcctgt ggattgttat tactcgcggc ccagccggcc 40
 atgacgagg ttacgcttca gcagtcctga cctgagctgg tgaagccggg ggcttcagtg 120
 aagatttcct gcaaaagctt tggtacgca ttcagtagct ctgggatgaa ctgggtgaag 160
 cagaggcctg gacagggtct tgagtggatt ggaaggattt atcctggaaa tggagatact 200
 aactacaatg ggaagttcaa gggcaaggcc acactgaact cagacaaaac ctccagpaca 240
 gctacatgc agctcagcag cctgacctct gtggaacttg cgtctatatt ctgtgcagat 280
 ggtaacgtat attactatgc tatggactac tggggtcaag gaacctcagt caccgtctcc 320
 tcaggtggag ggggttcagg tggggcgccc tctggcggtg ggggatgcaa aattgtcttc 360
 acccagtttc ctgcttcctt agctgtatct ctgggcaga gggccaccat ctcatgcagg 400
 gccagcaaaa gtgtcagtac atctggctat agttatatgc actggtacca acagaaacca 440

ggacagccac ccaaaactcct catctatctt gcatcacaac tagaatctgg ggtccctgac 101
 aggttcagtg gaagtgggtc tgggacagac ttacccctca acatccatcc tctggaggag 121
 gaggatgctg caacctatta ctgtcagcac agtagggagc ttctctggac gttctgggga 141
 ggcaccaaagc tggaaatcaa acgggggggc gcagaacaaa aactcatctc agaagaggt 161
 ctgaatggg gggacatca ccatcaccat cactaa 176

<210> 192

<211> 221

<212> IRT

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence:scFv region

<400> 102

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
 1 5 10 15

Ala Gln Pro Ala Met Ala Glu Val Gln Leu Gln Gln Ser Gly Pro Glu
 20 25 30

Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
 35 40 45

Tyr Ala Phe Ser Ser Ser Trp Met Asn Trp Val Lys Gln Arg Pro Gly
 50 55 60

Gln Gly Leu Glu Trp Ile Gly Arg Ile Tyr Pro Gly Asn Gly Asp Thr
 65 70 75 80

Asn Tyr Asn Gly Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys
 85 90 95

Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Val Asp
 100 105 110

Ser Ala Val Tyr Phe Cys Ala Asp Gly Asn Val Tyr Tyr Tyr Ala Met
 115 120 125

Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr Val Ser Ser Gly Gly Gly
 130 135 140

Gly Ser Gly Gly Arg Ala Ser Gly Gly Gly Gly Ser Gln Ile Val Leu
 145 150 155 160

Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala Thr
 165 170 175

Ile Ser Cys Arg Ala Ser Lys Ser Val Ser Thr Ser Gly Tyr Ser Tyr
 180 185 190

Met His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
 195 200 205

Tyr Leu Ala Ser Asn Leu Glu Ser Gly Val Pro Ala Arg Phe Ser Gly
 210 215 220

Ser Gly Ser Gly Thr Asp Phe Thr Leu Asn Ile His Pro Val Glu Glu
 225 230 235 240

Glu Asp Ala Ala Thr Tyr Tyr Cys Gln His Ser Arg Glu Leu Pro Arg
 245 250 255

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg Ala Ala Ala Glu
261 265 271

Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala His His His
275 280 285

His His His
290

<210> 103
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> Description of the artificial sequence:primer

<400> 103
gggggcagaa caaaaactca tctcagaaga ggtatgaat ggggcggcac atcaccatca 60
cctcaactaa taag 74

<210> 104
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<221> Description of the artificial sequence:primer

<400> 104
ttattagtga tggatgatgt gatgtgccgc cccattcaga tctctctctg agatgagttt 60
tggctctgc 69

<210> 105
<211> 15
<212> FRT
<213> Artificial Sequence

<220>
<221> Description of the artificial sequence:CDR3 region

<400> 105
Cys Xaa Xaa Tyr Gly Asn Ser Pro Lys Gly Phe Ala Tyr Xaa Xaa Cys
1 5 10 15

<210> 106
<211> 16
<212> FRT
<213> Artificial Sequence

<220>
<221> Description of the artificial sequence:CDR3 region

<400> 106
Phe Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asx
1 5 10 15